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I protein - protein search, using sw model										
Run on: May 15, 2006, 13:26:41 ; Search time 190 Seconds (without alignments)										
			2594.647 Million cell updates/sec							
file:	US-10-602-441-4	effect score:	5901							
sequence:	1 MTRAPRCPAVRSLLRSRYE.....TILKAAADPALSDFQFTLID 1122	oring table:	BLOSUM62							
Gapop 10.0 , Gapext 0.5	2443163 seqs, 439378781 residues	total number of hits satisfying chosen parameters:	2443163							
Minimum DB seq length: 0	Maximum DB seq length: 2000000000	Minimum DB seq length: 0	Maximum DB seq length: 2000000000							
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries										
A_Geneseq_21:*										
1: GeneseqP1900:*										
2: GeneseqP1900:*										
3: GeneseqP2004:*										
4: GeneseqP2004:*										
5: GeneseqP2004:*										
6: GeneseqP2003:*										
7: GeneseqP2003:*										
8: GeneseqP2004:*										
9: GeneseqP2005:*										
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.										
SUMMARIES										
result No.	Score	Match	Length	DB ID	Query	Score	Match	Length	DB ID	Description
1	5901	100.0	1122	2	AAY26579	Aay26579 Murine telomerase reverse transcriptase (mTERT) enzyme				
2	5901	100.0	1122	8	ADG90601	Adg90601 Murine telomerase reverse transcriptase (mTERT) enzyme				
3	5854	99.2	1122	5	ABR06711	Abbr06711 Mouse telomerase reverse transcriptase (mTERT) enzyme				
4	4859	82.3	1152	8	ADG90609	Adg90609 Murine telomerase reverse transcriptase (mTERT) enzyme				
5	4751	80.5	1128	4	ADD21416	Add21416 Golden hamster telomerase reverse transcriptase (mTERT) enzyme				
6	4751	80.5	1128	8	ADG90603	Adg90603 Hamster telomerase reverse transcriptase (mTERT) enzyme				
7	3505	59.4	1132	2	AAY46957	Aay46957 Human telomerase reverse transcriptase (mTERT) enzyme				
8	3505	59.4	1132	2	AAW90251	Aaw90251 Human cat telomerase reverse transcriptase (mTERT) enzyme				
9	3505	59.4	1132	2	AAY28881	Aay28881 Human telomerase reverse transcriptase (mTERT) enzyme				
10	3505	59.4	1132	2	AAY32090	Aay32090 Human telomerase reverse transcriptase (mTERT) enzyme				
11	3505	59.4	1132	2	AAY43621	Aay43621 A human telomerase reverse transcriptase (mTERT) enzyme				
12	3505	59.4	1132	2	AAY26580	Aay26580 Human telomerase reverse transcriptase (mTERT) enzyme				
13	3505	59.4	1132	4	ARC64859	Arc64859 Human telomerase reverse transcriptase (mTERT) enzyme				
14	3505	59.4	1132	4	AAG64329	Aag64329 Human telomerase reverse transcriptase (mTERT) enzyme				
15	3505	59.4	1132	4	AAB99930	Aab99930 Human telomerase reverse transcriptase (mTERT) enzyme				
16	3505	59.4	1132	4	AAB82765	Aab82765 Human telomerase reverse transcriptase (mTERT) enzyme				
17	3505	59.4	1132	5	AAB29226	Aab29226 Human telomerase reverse transcriptase (mTERT) enzyme				
18	3505	59.4	1132	5	AAU7235	Aau7235 Human telomerase reverse transcriptase (mTERT) enzyme				
19	3505	59.4	1132	6	ABR42384	Abr42384 Human telomerase reverse transcriptase (mTERT) enzyme				
20	3505	59.4	1132	6	ABR42063	Abr42063 Human telomerase reverse transcriptase (mTERT) enzyme				
21	3505	59.4	1132	6	ABP56676	Abp56676 Human telomerase reverse transcriptase (mTERT) enzyme				
22	3505	59.4	1132	6	ABP58045	Abp58045 Human telomerase reverse transcriptase (mTERT) enzyme				
23	3505	59.4	1132	7	ADD21420	Add21420 Human telomerase reverse transcriptase (mTERT) enzyme				
24	3505	59.4	1132	7	ABD72743	Abd72743 Human telomerase reverse transcriptase (mTERT) enzyme				

XX	Sequence 1122 AA;	Db	961 KTMNKLLSVLRLKCHGLFLDLQVNSLQTVICINIVKIFLQAYRFHACVQLPFPQRVK 1020
SQ	Query Match 100.0%; Score 5901; DB 2; Length 1122;	Qy	1021 NLTPFLGILSSQASCCYAIKLUKVNQGHTLKAQSGSPPEAHMLCYQAFJLKAHSVYK 1080
	Best Local Similarity 100.0%; Pred. No. 0;	Db	1021 NLTPFLGILSSQASCCYAIKLUKVNQGHTLKAQSGSPPEAHMLCYQAFJLKAHSVYK 1080
Matches 1122; Conservative 0; Mismatches 0; Gaps 0;		Qy	1081 CLLGFLRATQKLCKRLPEATMTLKAADPALSTDQTILD 1.1.22
Qy	1 MTRAPRCPAVRSILRSRREYRPLATFVRRGPEGRRLVQGDPKTYRFLVQAQCLVCMW 60	Db	1081 CLLGFLRATQKLCKRLPEATMTLKAADPALSTDQTILD 1.1.22
Db	1 MTRAPRCPAVRSILRSRREYRPLATFVRRGPEGRRLVQGDPKTYRFLVQAQCLVCMW 60		
Qy	61 GSQPPPADLSFHQVSSKELVARYVORLCEERNVTLAFCFELLNEARGGPPMAPTSSVR 120		RESULT 2
Db	61 GSQPPPADLSFHQVSSKELVARYVORLCEERNVTLAFCFELLNEARGGPPMAPTSSVR 120	ADG90601	ADG90601 standard; protein; 1122 AA.
Qy	121 SYLPNTVETLTERVSGAMMLLSRVDLVLVLLAHCALYLLVPPSCAYQVCGSPLYQICA 180	XX	ADG90601;
Db	121 SYLPNTVETLTERVSGAMMLLSRVDLVLVLLAHCALYLLVPPSCAYQVCGSPLYQICA 180	XX	DT 25-MAR-2004 (first entry)
Qy	181 TTDIWPSSVASYRTPRTPVGRNFTNLPLQQIKKSSRQEAKPLAPSRTGTRHLSLTSTS 240	XX	Murine TERT SEQ ID NO:4.
Db	181 TTDIWPSSVASYRTPRTPVGRNFTNLPLQQIKKSSRQEAKPLAPSRTGTRHLSLTSTS 240	XX	DB mouse; immune response; telomerase reverse transcriptase; TERT;
Qy	241 VPSAKKRCRCPYPRVEGPHQVLPPSGKSWVPSPARSPVPTAEDLSSKGKVSDLSL 300	XX	KW mouse; immune response; telomerase reverse transcriptase; TERT;
Db	241 VPSAKKRCRCPYPRVEGPHQVLPPSGKSWVPSPARSPVPTAEDLSSKGKVSDLSL 300	XX	KW cytostatic; immunostimulant; cancer; cytotoxic T cell response.
Qy	301 SGSVCCRKHPSTSSTLSPRONAFOLRPFIETRPHLYSPRGQERLNPSFLSNIQPNLT 360	XX	OS Mus sp.
Db	301 SGSVCCRKHPSTSSTLSPRONAFOLRPFIETRPHLYSPRGQERLNPSFLSNIQPNLT 360	XX	XX
Qy	361 GARRLYEITIPLGSRPTSGPLCRTHRLSRYTQMRPLFQQLVNHAEQCTYRLRSHCRF 420	XX	PN WO2004002408-A2.
Db	361 GARRLYEITIPLGSRPTSGPLCRTHRLSRYTQMRPLFQQLVNHAEQCTYRLRSHCRF 420	XX	XX
Qy	421 RTANOOQTDAINTSPPHMIDLRLHSSPQVYQYGLPACLKVKVSAASLWGTGRHNERFFKVN 480	XX	08-JAN-2004.
Db	421 RTANOOQTDAINTSPPHMIDLRLHSSPQVYQYGLPACLKVKVSAASLWGTGRHNERFFKVN 480	XX	XX
Qy	541 TYVQQLRSRFFYTESTFQQRLLFFYRKSYWSKLSQIGVROHLERYRLRELQSEEVRHQ 600	XX	24-JUN-2003; 2003WO-US019844.
Db	541 TYVQQLRSRFFYTESTFQQRLLFFYRKSYWSKLSQIGVROHLERYRLRELQSEEVRHQ 600	XX	XX
Qy	601 DTLWAMPICLRLFPIKNGLPIVNMYSMGTALGRKQAOHTKTLFSLMNYERT 660	XX	27-JUN-2002; 2002US-0391295P.
Db	601 DTLWAMPICLRLFPIKNGLPIVNMYSMGTALGRKQAOHTKTLFSLMNYERT 660	XX	XX
Qy	661 KPHLMQSSVLMNDIYTRWTRAPVLRVALLQTPRMVYKADVTGAYDA.PQGKLVYVVA 720	XX	(GERO-) GERON CORP.
Db	661 KPHLMQSSVLMNDIYTRWTRAPVLRVALLQTPRMVYKADVTGAYDA.PQGKLVYVVA 720	XX	XX
Qy	721 NMIRHSESTYCIROYAVRDRDSQGQYHKSFRQVTTLSDQYMGFLRQLQDSASALR 780	XX	PI Majundar A, Perber IA, Frolkis M, Wang Z;
Db	721 NMIRHSESTYCIROYAVRDRDSQGQYHKSFRQVTTLSDQYMGFLRQLQDSASALR 780	XX	XX
Qy	781 NSVVIQOSISMNESSSFEDPFLHFLRHSVYKIGDRCYTOCGIPIQGSISLTLCSLCFG 840	XX	WPI 2004-071946/07.
Db	781 NSVVIQOSISMNESSSFEDPFLHFLRHSVYKIGDRCYTOCGIPIQGSISLTLCSLCFG 840	XX	DR N-PSDB; ADG90600.
Qy	841 DMENKLFAEVQDGLLRFVDDFLLTTPHDQAKTSLSTLVGVPYEGCMINLQKTVNF 900	XX	PS Claim 10; SEQ ID NO 4; 44pp; English.
Db	841 DMENKLFAEVQDGLLRFVDDFLLTTPHDQAKTSLSTLVGVPYEGCMINLQKTVNF 900	XX	XX
Qy	901 PVEPGTIGGAAQYQLPAHCLPWPWCGLILDTQTLFCDYSGYAQTSIKTSITFQSFKAG 960	XX	CC The invention relates to a novel method for eliciting an immune response in a mammal subject that is specific for its own telomerase reverse transcriptase (TERT), comprising administering an immunogenic composition containing a protein with at least 20 consecutive amino acids of TERT of another mammal species, or a nucleic acid encoding the protein. A composition of the invention has cytostatic, and immunostimulant activity. The protein or the nucleic acid encoding the protein is useful in the manufacture of a medicament for the treatment of cancer in a human or for eliciting a cytotoxic T cell response in a human.
Db	901 PVEPGTIGGAAQYQLPAHCLPWPWCGLILDTQTLFCDYSGYAQTSIKTSITFQSFKAG 960	XX	CC
Qy	961 KTMNKLLSVLRLKCHGLFLDLQVNSLQTVICINIVKIFLQAYRFHACVQLPFPQRVK 1020	XX	CC
Db	961 KTMNKLLSVLRLKCHGLFLDLQVNSLQTVICINIVKIFLQAYRFHACVQLPFPQRVK 1020	XX	CC
Qy	100.0%; Score 5901; DB 8; Length 1122;	Qy	1 MTRAPRCAVRSILSRYREVWPLNTFVRIGPESRRLYQGDPKTYRFLVQOCLVCMHW 60
Db	Best Local Similarity 100.0%; Pred. No. 0; Mis matches 0; Indels 0; Gaps 0;	Db	1 MTRAPRCAVRSILSRYREVWPLNTFVRIGPESRRLYQGDPKTYRFLVQOCLVCMHW 60
Matches 1122; Conservative 0; Mismatches 0; Gaps 0;		Qy	61 GSQPPPADLSFHQSLSKELVARYVQRLCERNERNVLAFCFELLNEARGGPPMAPTSSVR 120
Qy	1 PVEPGTIGGAAQYQLPAHCLPWPWCGLILDTQTLFCDYSGYAQTSIKTSITFQSFKAG 960	Db	61 GSQPPPADLSFHQSLSKELVARYVQRLCERNERNVLAFCFELLNEARGGPPMAPTSSVR 120
Db	1 PVEPGTIGGAAQYQLPAHCLPWPWCGLILDTQTLFCDYSGYAQTSIKTSITFQSFKAG 960	Qy	121 SYLPNTVETLVRSSAWMILSRVYDDLLVLLAHCALYLLVPPSCAYQVCGSPPLQICA 180

Db	121	SYLBNNTVETLRVSGAMMILLSRVGDLLVILLAHCAIYLVPPSCAYQVCGSPLYQICA	180	XX	11-JUN-2002	(first entry)
Qy	181	TTDIWPSIYSTASRTRPGRNFTNLRFQQIKSSSRQAPKPLALPERGTRKHLSTSTS	240	XX	DE	Mouse telomerase protein sequence.
Db	181	TTDIWPSIYSTASRTRPGRNFTNLRFQQIKSSSRQAPKPLALPERGTRKHLSTSTS	240	XX	RW	Mouse; telomerase; promoter; telomerase catalyst subunit; TERT; mTERT;
Qy	241	VPSAKKACRYPVVESECPHQVLTPTSGKSMWPSPARSPEVPTAEDLSSKGKVDSL	300	XX	KW	enzyme; transgenic mouse; drug development; anticancer.
Db	241	VPSAKKACRYPVVESECPHQVLTPTSGKSMWPSPARSPEVPTAEDLSSKGKVDSL	300	OS	XX	Mus sp.
Qy	301	SGSVCCRKPKPSSTSLLSPRONAFOLRPFIELTRFLYSLRGDQERLNPFLSNLQPNLT	360	XX	XX	JP200200121-A.
Db	301	SGSVCCRKPKPSSTSLLSPRONAFOLRPFIELTRFLYSLRGDQERLNPFLSNLQPNLT	360	XX	XX	08-JUN-2002.
Qy	361	GARRLVEITLGSRPRTSGPLCRTHRLSRRYQMRPLFQQLVNNHACQYTRLLRSHCRF	420	XX	XX	23-JUN-2000; 2000JP-00190137.
Db	361	GARRLVEITLGSRPRTSGPLCRTHRLSRRYQMRPLFQQLVNNHACQYTRLLRSHCRF	420	XX	XX	PR 2000JP-00190137.
Qy	421	RTANQVTDALNTSPPHMIDLRLHSSWQVNGFLRACLKTVVASLWGTTRNERRPKN	480	XX	PA	(RIKO-) ZH RIKOGAKU SHINKOKAI.
Db	421	RTANQVTDALNTSPPHMIDLRLHSSWQVNGFLRACLKTVVASLWGTTRNERRPKN	480	XX	PA	(KIRI) KIRIN BREWERY KK.
Qy	481	LKKPISLGKYGKLSQBLMWKQVEDCWLWRSPPGKDRVPAEHRRLRERILATFLWLM	540	XX	XX	WPI: 2002-298275/34.
Db	481	LKKPISLGKYGKLSQBLMWKQVEDCWLWRSPPGKDRVPAEHRRLRERILATFLWLM	540	XX	XX	A transgenic mouse comprising a DNA promoter region of mouse telomerase catalyst subunit (TERT) is used for the development of drugs and anticancer agents for regeneration of tissues and organs.
Qy	541	TYVYQVLLRSFFYITESTEYQKPLFYTYSVNEKSYKQVQHLLERVLRLELSQEEYTRHQ	600	XX	XX	Disclosure: Fig 3: 13PP; Japanese.
Db	541	TYVYQVLLRSFFYITESTEYQKPLFYTYSVNEKSYKQVQHLLERVLRLELSQEEYTRHQ	600	CC	CC	The present invention describes a transgenic mouse (1) comprising a DNA catalyst subunit (TERT) and a DNA containing a promoter region of mouse telomerase connected under the control of the promoter region. The transgenic mouse can be used in the development of drugs and anticancer agents for regeneration of tissues and organs. The present sequence represents the mouse telomerase protein, which is given in the exemplification of the present invention
Qy	601	DTWAMPICRLRPIPKNGLRLPVNMSYSMGFRALGRKQAOQHTPQLKTLFSMLNVERT	660	CC	CC	PS Disclosure: Fig 3: 13PP; Japanese.
Db	601	DTWAMPICRLRPIPKNGLRLPVNMSYSMGFRALGRKQAOQHTPQLKTLFSMLNVERT	660	CC	CC	The present invention describes a transgenic mouse (1) comprising a DNA catalyst subunit (TERT) and a DNA containing a promoter region of mouse telomerase connected under the control of the promoter region. The transgenic mouse can be used in the development of drugs and anticancer agents for regeneration of tissues and organs. The present sequence represents the mouse telomerase protein, which is given in the exemplification of the present invention
Qy	661	KPHLMGSSVGLANDIVTRWTRAFVLRVYALDQTPTMVFKAUTGVAYDAIPOGKLVYEVVA	720	CC	CC	Sequence 1122 AA;
Db	661	KPHLMGSSVGLANDIVTRWTRAFVLRVYALDQTPTMVFKAUTGVAYDAIPOGKLVYEVVA	720	CC	CC	Sequence 1122 AA;
Qy	721	NMTRHSESTTCYCRQAYTRVDRSDQCVHKSFRQQVTTSLDQYQMGPLKHLQDSDASLR	780	XX	XX	Query Match 99.2%; Score 5854; DB 5; Length 1122;
Db	721	NMTRHSESTTCYCRQAYTRVDRSDQCVHKSFRQQVTTSLDQYQMGPLKHLQDSDASLR	780	Db	Db	Best Local Similarity 99.4%; Pred. No. 0; Matches 1115; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy	781	NSVIEQSISSMNESSSSLFDFPLHLRHSVVKIGDRCTYQCOGIPQCSLSSLICSLCFG	840	Qy	1	MTRAPCPAVSLLRSRSPYEWPLATFVRLGSPGRARLVPQGDPKPYRTLVAQCLVCMHW 60
Db	781	NSVIEQSISSMNESSSSLFDFPLHLRHSVVKIGDRCTYQCOGIPQCSLSSLICSLCFG	840	Db	1	MTRAPCPAVSLLRSRSPYEWPLATFVRLGSPGRARLVPQGDPKPYRTLVAQCLVCMHW 60
Qy	841	DMEKLKFABVQRDGLLRFVDDFLVTPHLDQAKTFLSTLHVGPVEYGMINLQKTVNF	900	Qy	61	GSQPAPPDSLPHQVSSSLKELYARVWLCERNERNVLAFGFELLNEARGGPMPMTSSVR 120
Db	841	DMEKLKFABVQRDGLLRFVDDFLVTPHLDQAKTFLSTLHVGPVEYGMINLQKTVNF	900	Db	61	GSQPAPPDSLPHQVSSSLKELYARVWLCERNERNVLAFGFELLNEARGGPMPMTSSVR 120
Qy	901	PYEPGTLGQGAAPQLPACFLFWPGCLLDTQTLTLEFVCDYQTAQTSKSLTFOQYKAG	960	Qy	121	SYLNPNTVETLRVSGAMMILLSRVGDLLVYLALCALYLLVPPSCAYQVCGSPLYQICA 180
Db	901	PYEPGTLGQGAAPQLPACFLFWPGCLLDTQTLTLEFVCDYQTAQTSKSLTFOQYKAG	960	Db	121	SYLNPNTVETLRVSGAMMILLSRVGDLLVYLALCALYLLVPPSCAYQVCGSPLYQICA 180
Qy	961	KTMRNKLISVLRLKCHGFLDQVNISLQTVCINIKYKFLQYRHFACVQIQLPFDVRK	1020	Qy	181	TTDIWPSVSAYRPTPVGRAFTNRLQQIKSSSQQAPKPLLRSRGTRKHLSTSTS 240
Db	961	KTMRNKLISVLRLKCHGFLDQVNISLQTVCINIKYKFLQYRHFACVQIQLPFDVRK	1020	Db	181	TTDIWPSVSAYRPTPVGRAFTNRLQQIKSSSQQAPKPLLRSRGTRKHLSTSTS 240
Qy	1021	NLTFFGTTISSQASCYAILKVKPQGMTLKAGSFPPBAAHWLYCQAFLLKLAAHSYVYK	1080	Qy	241	VPSAKKACRYPVPRREGPHQVLPTPSGKSWVPSPARSPVPTAKDLSRGKVKSDLSL 300
Db	1021	NLTFFGTTISSQASCYAILKVKPQGMTLKAGSFPPBAAHWLYCQAFLLKLAAHSYVYK	1080	Db	241	VPSAKKACRYPVPRREGPHQVLPTPSGKSWVPSPARSPVPTAKDLSRGKVKSDLSL 300
Qy	1081	CJLGPTAQQKLLCRKLFPEATMILKAADPAUSTDFQTLID 1122		Qy	301	SGSVCCRKPKPSSTSLLSPRONAFQLPRTPLCRTLRSRQYQPLFQQLVNNHACQYTRLLSHCRF 420
Db	1081	CJLGPTAQQKLLCRKLFPEATMILKAADPAUSTDFQTLID 1122		Db	301	SGSVCCRKPKPSSTSLLSPRONAFQLPRTPLCRTLRSRQYQPLFQQLVNNHACQYTRLLSHCRF 420
AC	AC		Qy	361	GARRLVEITLGSRPRTSGPLCRTRLSHRQWQMLPFLQQLVNNHACQYTRLLSHCRF 420	
XX	XX		Db	361	GARRLVEITLGSRPRTSGPLCRTRLSHRQWQMLPFLQQLVNNHACQYTRLLSHCRF 420	
AC	AC		Qy	421	RTANQVTDALNTSPPHMIDLRLHSSWQVNGFLRACLKTVVASLWGTTRNNEERFPKN 480	

RESULT 3  
ABB06711  
ID ABB06711 standard; protein: 1122 AA.  
XX  
AC

Db	421	RTANQYTDALNTSPPHMDLRLRISSPQWQYGF.RACLCXVVSASLWGRTRNENRFFCN	480	PI Majumdar A, Ferber IA, Frolkis M, Wang Z; XX XX DR WPI: 2004-071946/07.
Qy	481	LKKFISIGKIGLSSLBLWAKMKVEDCHWLRSSPGKDRPAAEHLRERLATEFLWFLD	540	PT Eliciting an immune response in a mammal specific for its own telomerase
Db	481	LKKFISIGKIGLSSLBLWAKMKVEDCHWLRSSPGKDRPAAEHLRERLATEFLWFLD	540	PT reverse transcriptase (TERT), useful for treating or preventing cancer,
Qy	541	TYVQQLRSPPFYTTESTFKQRLFFYKRSWKSLSQIGVQHLRVRRLSQQEVHQ	600	PT comprises administering a composition containing TERT of another
Db	541	TYVQQLRSPPFYTTESTFKQRLFFYKRSWKSLSQIGVQHLRVRRLSQQEVHQ	600	PT mammalian species.
Db	541	TYVQQLRSPPFYTTESTFKQRLFFYKRSWKSLSQIGVQHLRVRRLSQQEVHQ	600	XX Claim 10; SEQ ID NO 12; 44PP; English.
Qy	601	DTWLAMPICRLRFLPKPQNGRPIVNMYSMGRKQAHQFLRKLFSMLNVERT	660	XX
Db	601	DTWLAMPICRLRFLPKPQNGRPIVNMYSMGRKQAHQFLRKLFSMLNVERT	660	CC The invention relates to a novel method for eliciting an immune response
Qy	661	KPHFLMGSSVLGMNDIYTRWAPFLVRLRQALDQTPMVFADTVGAYDA.PQGKLUVEVA	720	CC in a mammalian subject that is specific for its own telomerase reverse
Db	661	KPHFLMGSSVLGMNDIYTRWAPFLVRLRQALDQTPMVFADTVGAYDA.PQGKLUVEVA	720	CC transcriptase (TERT), comprising administering an immunogenic composition
Qy	721	NMIRHSESTYCTROYAVVRRDSQGQVHSFRRQVTLSLQDYMQFLKQDSDASLR	780	CC containing a protein with at least 20 consecutive amino acids of TERT of
Db	721	NMIRHSESTYCTROYAVVRRDSQGQVHSFRRQVTLSLQDYMQFLKQDSDASLR	780	CC another mammalian species, or a nucleic acid encoding the protein. A
Qy	781	NSVVIQOSISNNNESSLDFFLHFLRHSYVKIGDRCYTOCGI.PQGSISLJCSLCFG	840	CC composition of the invention has cytotoxic, and immunostimulant
Db	781	NSVVIQOSISNNNESSLDFFLHFLRHSYVKIGDRCYTOCGI.PQGSISLJCSLCFG	840	CC activity. The protein or the nucleic acid encoding the protein is useful
Qy	841	DMENKLPAFAYVQDGLLRFVDDFLFLYVTPHLDQARTFLSLVYHGPEYGMINLQKTVNF	900	CC in the manufacture of a medicament for the treatment of cancer in a human
Db	841	DMENKLPAFAYVQDGLLRFVDDFLFLYVTPHLDQARTFLSLVYHGPEYGMINLQKTVNF	900	CC or for eliciting a cytotoxic T cell response in a human.
Qy	901	PVEPGTIGGAAPYQPLPAHCLPFWCGNLLDTOTLEVFLQDVGAYQTSIKSLTFSQVFKAG	960	XX Sequence 1152 AA;
Db	901	PVEPGTIGGAAPYQPLPAHCLPFWCGNLLDTOTLEVFLQDVGAYQTSIKSLTFSQVFKAG	960	Query Match 62.3%; Score 4859; DB 8; Length 1152;
Qy	961	KTMRNLKLSVTLRKCHGLFLDLQVNSLQTYCINIKYKFLQAYRPHACTVQPLPFDQYRK	1020	Best Local Similarity 83.2%; Pred. No. 0;
Db	961	KTMRNLKLSVTLRKCHGLFLDLQVNSLQTYCINIKYKFLQAYRPHACTVQPLPFDQYRK	1020	Matches 955; Mismatches 40; Indels 32; Gaps 7;
Qy	1021	NLTFFLGIISSQASCCYALKVNKPMTLXASGSFPEAAHVLQYQFLKLAHHSVYK	1080	Qy 1 MTRAPRCPAVSLRSLRSYREVWPLATFVRLGPGRGLRQVQGPDKTIRTLYAQCLVCMHN 60
Db	1021	NLTFFLGIISSQASCCYALKVNKPMTLXASGSFPEAAHVLQYQFLKLAHHSVYK	1080	Db 1 MTRAPRCPAVSLRSLRSYREVWPLATFVRLGPGRGLRQVQGPDKTIRTLYAQCLVCMHN 60
Qy	1081	CLLGPLRTAQKLLCRKLPATEMTLKAADPALSTDQFLD	1122	Qy 61 GSQPPADLFSHQVSISLKELVARYVQRLCERNEENVILAFGFELINEARQGPMAFTSSV
Db	1081	CLLGPLRTAQKLLCRKLPATEMTLKAADPALSTDQFLD	1122	Db 61 GARPPAASFSHQVSISLKELVARYVQRLCERNEENVILAFGFELINEARQGPMAFTSSV
Qy	241	VPSAKKARCYPVPRVEGPHQVLPITPSGSKWSWTPSPARSPEVP	297	Qy 120 SYLPNTVITELTRVSGAMMILLSRVGDYLIVLLAHCALYLYPPS CAYOVCGSPLYQICIA 180
Db	241	VPSAKKARCYPVPRVEGPHQVLPITPSGSKWSWTPSPARSPEVP	297	Db 120 SYLPNTVITELTRVSGAMMILLSRVGDYLIVLLAHCALYLYPPS CAYOVCGSPLYQICIA 180
Qy	298	LSLSGSVCCCKHKSPPSISLSPRQNAFOLRP	300	Qy 181 TTDIWPSSIASYRTRPGRNFTNLRELQKIKSSRQEAPKPLALPSRTKHLSTLSTS 240
Db	298	LSLSGSVCCCKHKSPPSISLSPRQNAFOLRP	300	Db 181 TTOARPPPHASGRPRPGRNFTNLGFCAWRNNSVREAGVPLGQPSPEAKRGSASRS 240
Qy	301	LSLSGSVCCCKHKSPPSISLSPRQNAFOLRP	359	Qy 241 VPSAKKARCYPVPRVEGPHQVLPITPSGSKWSWTPSPARSPEVP
Db	301	LSLSGSVCCCKHKSPPSISLSPRQNAFOLRP	359	Db 241 LPLPKKARIGAAPEPERTPTVQGSWSWTPSCTRTRVPSDAGSPVVSPPARPEEDLSKKGKVSD 297
Qy	356	QPNUTGARLVEIIFLGSRSPRTSPLCPTHLRSPRYWQRLPFCQULLVNAECOYRVLR	415	Db 356 QPSLITGARLVEIIFLGSRPTWPSCLCRTHLSSRYYWQRLPFCQULLVNAECOYRVLR 419
Db	360	QPSLITGARLVEIIFLGSRPTWPSCLCRTHLSSRYYWQRLPFCQULLVNAECOYRVLR	419	Qy 416 SHCRERTANQVTDALNTSPP
Qy	416	SHCRERTANQVTDALNTSPP	455	Db 420 SHCPRAAATPVAGAINTSPQGSVAPEVAPEQEQTDSTRNLQHSSPQVYGPL 455
Db	420	SHCPRAAATPVAGAINTSPQGSVAPEVAPEQEQTDSTRNLQHSSPQVYGPL	455	Qy 456 RACICKVYASLNGTRHNERFFKQNLKCPFISLGRKXGKLSLQELWMKQYEDCHWLRSSPG 515
Qy	456	YESVEAEEHLRERLRLAKEHPLFLWLMSTYVVEILRSPPVITEETFQKNRLFFYRKSWS 599	Db 480 RACICKVYASLNGTRHNERFFKQNLKCPFISLGRKXGKLSLQELWMKQYEDCHWLRSSPG 515	
Db	516	KDRIWAEEHLRERLRLAKEHPLFLWLMSTYVVEILRSPPVITEETFQKNRLFFYRKSWS 572	Qy 516 KDG90609 Standard: protein: 1152 AA.	
Qy	540	YESVEAEEHLRERLRLAKEHPLFLWLMSTYVVEILRSPPVITEETFQKNRLFFYRKSWS 599	AC ADG90609;	
Db	540	YESVEAEEHLRERLRLAKEHPLFLWLMSTYVVEILRSPPVITEETFQKNRLFFYRKSWS 599	DT 25-MAR-2004 (first entry)	
Qy	573	KLQSTIGVROHLERYLRLRELSQEEYRHQDWTWAMPICRLRIPKPKGLRPIVNMYSMGT	632	DE TERT consensus sequence SEQ ID NO:12.
Db	600	KLQSTIGVROHLERYLRLRELSQEEYRHQDWTWAMPICRLRIPKPKGLRPIVNMYSMGT	632	KW immune response; telomerase reverse transcriptase; TERT; cytostatic;
Qy	633	RALGRKQAOHFTORLKLTSMLNAYERTKPHLMSGNDTYRTWFAFLVRALDQ 692	XX	KW immunostimulant; cancer; cytotoxic T cell response.
Db	633	RALGRKQAOHFTORLKLTSMLNAYERTKPHLMSGNDTYRTWFAFLVRALDQ 692	XX	OS Unidentified.
PW	W02004002408-A2.	XX	XX	
XX	:	XX	XX	
AC	ADG90609;	XX	XX	
PD	08-JAN-2004.	XX	XX	
PP	24-JUN-2003; 2003WO-US019844.	XX	XX	
PR	27-JUN-2002; 2002US-0393295P.	XX	XX	
PA	(GERO-) GERON CORP.	XX	XX	

660	RRAFGRKQKQHFTQQLKTLFSLVNEYTKPHPLLGASVLGNDITIRTWTPLVRLRPLDP	719
693	TPRMFYKFTADTYGDAIPQKLVVEYANMIRHSESTCYTROYAVYVYRDSQGQVHKSFR	752
720	TPRMFYKFTADTYGDAIPQKLVVEYANMIRHSESTCYTROYAVYVYRDSQGQVHKSFR	779
753	QVTTLSLDQPYMCQFLKHLQDSALRNSVYEQSISMNESSSLFDPFLHPLHSVVK	812
780	QVSTTLSLDQPYMCQFLKHLQDSALRNSVYEQSISLNERSASSLFDFFPLRFLHSVVK	839
813	IGDPCYTQCGIPGQSSLSTLCSLCFGDMENKLFAVQRDGLLRLRVDPFLVTPHLDQ	872
840	IGGRCVYQCGIPGQSSLSTLCSLCFGDMENKLFAVQRDGLLRLRVDPFLVTPHLDQ	899
873	AKTFLSTLVHGVPBEGCMINLQKTVNFPVPBEPOTLGGAAPYOLPAHCLPFCGMLLDTQT	932
900	AKTFLSTLVGRVDPBEGCMINLQKTVNFPVPBGTIGSTAPTOPLAHLCPFCGMLLDTQT	959
933	LEVFCDYSGYAQTSIKTSITRQSPVAKGKTMANKLISVRLKCHGFLDLOQNSL-QrvcI	992
960	LEVFCDYSGYARTSIKASLTFQRFVAKGKMNENKLISVRLKCHSFLDLOQNSL-QrvcI	1019
993	NIYKIFLQAYRPHACVQLPFPQRVRVKNTFLGISSQASCCYAILKVRNPQGTLK--	1052
1020	NIYKIFLQAYRPHACVQLPFPQRVRKNTFLGISSQASCCYAILKVRNPQGTLK	1079
1051	-ASGFFPDEAAHWLYCYQAFLLKLAHSVYTKCILGPLRTAQKLICRKLPEATMTLKA	1105
1080	GAAGFFPDEAAHWLYCYQAFLLKLAHSVYTKCILGPLRTAQQLCRKLPEATMTL	1134
1110	DPAISTDQQTLL	1122
1140	DPAISTDQQTLL	1152

PN	WO2003044169-A2.
XX	
ED	30-MAY-2003.
XX	
PP	15-NOV-2002; 2002WO-US036729.
XX	
PR	15-NOV-2001; 2001US-0334760P.
XX	
PA	(UTEM ) UNIV TEMPLE.
XX	
PI	Reddy PE, Rane SG, Mettus RV;
XX	
DR	WPP; 2003-449813/42.
XX	
PT	A composition for reversibly inducing continual growth in normal cells comprises a cyclin dependent kinase protein (e.g. cdk4, cdk2 or cdk6) or its active fragment, derivative, homolog or analog, having an activating mutation.
PT	
PS	Disclosure; Page 119-121; 77pp; English.
XX	

1	MTTPAPRCDAVRSILRSRSPBWWPLATPWRILGPRCBRPLQPGDPKLYPTPLVAQQLCJCMHN	60
1	MPPAPCRAVALLRSQTRQWPPLATPWRILGPRCBRPLQPGDPKLYPTPLVAQQLCJCMHN	60
61	GSQPPPADLSFHOVSISLKELVARYVQLCERNBNVLAQFPLBLNARGGPPMFTSSVR	120
61	DSQPPPADLSFHOVSISLKELVARYVQLCERNBNVLAQFPLBLNARGGPPMFTSSVR	120
121	SYLPLNTVETLRLVSGAMMLLSRVDGDLILVLLAHICALYLVPPSCAYQVCGSPLYQICA	180
121	SYLPLNTVETLRLVSGAMMLLSRVDGDLILVLLAHICALYLVPPSCAYQVCGSPLYQICA	180
181	TTDIWPSSASATPRTPGRNFTNLFLQOKKSRSQRQBAKPLAFLDSRGTKRHLITSTS	240
181	TAETWPSSVTRTPRTPGRNFTNLFLGSTRVRSNSHQBAAWKPPPLPSREAKRSLSLTNR	240
241	VPSAKARCYPVERBEPHROVLPPTSGCKWSPSPARSBEPV--.TAKBDLSSGKVS	297
241	VPSKAKRCDLAPLKEKDPYRQAQPTPSKTKWVDPNPKSHAVPIRPTKEDLSSGKVS	300
298	LSTLGSVYCKHKPSSSTSLSPPRONAFLQRLPFLTTRHFLYPSRGDGQEBRNLPSFLISNLQP	357
358	NLTGARLVEIIFLGSRPRTSGQLCORTAHLRSRQWQMRPLFQQLVHACQVYVLLRSH	417
361	SLTGARRIVELVFLGMRPRTSGPCKGRRRLSKYWMQRPLFQQLVHACRCPYVYVLLRSH	420
418	CRFRTANQVTDALN-TSPPHLMDLRLHSSPKYQYGFRLRACLCKVVSASLMGTRHEINBR	476
421	CRFRTAHQVAGLNTTSPQRLANLRLHSSPKYQYGFRLQACVGLVPPGJWSRHNRQ	480
477	FPQNLKKPPTISLGKYGKLSLQELAKWQKMDVCHNLASSPKDRVPPAEEHRLBRLLATELP	536
481	PPQNKRTSPKGDYKDLKSLQELTMKQVQDCRNLRSPPGNCVPAEEHRTTERILAVFLP	540
537	WLMDDTYVQLRSFPPYITESTFQKRLPPYRKTSWKLQJGVRQHLLRVLRLRSQBEV	596
541	WLMDDAYVLLRSFPPYITESTFQKRLPPYRKTSWRLQJGVRHLLRVLRLSQBEV	600
597	REHQDTWLMPCRLRFLPKPGNGRPTYNNMSGNCTRALGRKQKQAHFTORLKTLSMLN	656
601	RQRQEANPAMPICRLLRFLPKPSGRPIVMSY-MGTRAPDQGKQPHFTQCLTKTLSVLN	659
657	YERTKPHLMGSSVYLGNDIYRTWRAFLYRVLRAFLQDQTPMYFVZDVTGAYDAIPQGKLY	716
660	YELTKHTMLGASVGLNDIYRTWTRFLVRLTDPAPMRYFVZDVTGAYDAIPQDCLVY719	719



Db 9560 FKAGRNMRQKLLAVIRLKHSLFLDLQNSLQTCINVYKIFLQLQYRFRHACALQLPFDQ 1019  
 QY 10117 RVRKNLTFGLGISSQASCCYAILKVKNPGMTLK---ASGSFPEAAHMLCYOAFLKLAA 1073  
 Db 10120 HVRKNPAPFLSISNIASSCCYSLKVKAGMTLKAKGSIGSFPPEARLWLTQOAFLKLAA 1079  
 QY 1074 AHSTVYKCHGLGPARTAQKULCRKLPEATMILKAAADPALSTDFTQTLID 1122  
 Db 1080 GHSTVYKCHGLGPARTAQKULCRKLPEATMILKAAADPALSTDFTQTLID 1128

RESULT 7  
 AAW46957 ID AAW46957 standard; protein; 1132 AA.  
 XX AC AAW46957;  
 XX DTR 13-AUG-1998 (first entry)  
 XX DB Human telomerase reverse transcriptase.  
 XX KW Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;  
 KW cell proliferation; cancer; ageing; ribonucleoprotein.  
 OS Homo sapiens.  
 XX PN GB231791-A.  
 XX PD 08-APR-1998.  
 XX PP 01-OCT-1997; 97GB-00020890.  
 PR 01-OCT-1996; 96US-00724643.  
 PR 18-APR-1997; 97US-00844419.  
 PR 25-APR-1997; 97US-00846017.  
 PR 06-MAY-1997; 97US-00851843.  
 PR 09-MAY-1997; 97US-00854050.  
 PR 14-AUG-1997; 97US-00911312.  
 PR 14-AUG-1997; 97US-00912931.  
 PR 14-AUG-1997; 97US-00915533.  
 PA (GERO-) GERON CORP.  
 PA (UYTE-) UNTV TECHNOLOGY CORP.  
 PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;  
 PI Andrews WH;  
 XX WPI: 1998-171633/16.  
 DR N-PSDB, AAV2379.

XX Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing.

XX Claim 3: Fig 17; 387pp; English.

CC The present sequence represents human telomerase reverse transcriptase (hTRT), which is a ribonucleoprotein. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT by detecting the change in hTRT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein preparation of hTRT with a telomerase RNA component; (C) detection of the hTRT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT expression; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polynucleotide encoding hTRT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions

CC that are associated with high telomerase activity. A protein preparation of hTRT can also be used in the new methods

CC XX

CC SQ Sequence 1132 AA;

Query Match 59.4%; Score 3505; DB 2; Length 1132;  
 Best Local Similarity 62.4%; Pred. No. 0;  
 Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;

QY 1 MTRAPRCPEAVSILRSYREWPLAFVRLRGPGRVQEDPKYRTLVAQCLVCMW 60  
 1 MTRAPRCRAVRLRSYREVPLATEVRLGPGRVQGRLVQGRDPAFAFLVQCLVCPW 60

61 GSQPPPADLSSHQVSSKELKLYARVYVORLCENERNVLAQFPLLINEARGPPMFTSSV 120  
 61 DARPPPAAPSPRQVSCLKELYARVYVRLCERGAKVNLAFGFLALDARGGPPPEAFTPSV 120

QY 61 SYLNPNTVIEETURVSGIAWMLLSSRGDDLLVYLARCALYLVPPSCAYQVCGSPLYQICA 180  
 121 SYLNPNTVTDALRGSGAWGLLRRRGDDVVLVHLLARCALFVLYVAPSCAYQVCGSPLYQICA 180

181 TDIWPSVASYTRPTEPVGRFTNLRFLQQIKSSRQEQAPPLAFLPSRSRGTRHSLTSTS 240  
 181 ATQRPPPHAS GPRHRLG-----CERAWNHSYRBAQYPLGLAPGAAFRGGSASRS 231

QY 241 VPSAKKARCYPVPRVEGP-----HRQVLPLTPSGKSW-VPSPARSPVPTAERDLSK 292  
 232 LPLPKRPRRGAAPEPRTPTVCGSWAHPGTRGPSPDRGFCVYSPAR-----PAEATSL 286

QY 293 GRVSDLSLSS-GSVCKHKPKSSSTSLSSPRQNAFQLRP-FIETRHFILYSGRDPGQERBLNPSPF 350  
 287 GALSGTRHSHSPVGRHAGPPSTSRRPRPDTCPCEVIAETKHFYLISSGD-KEQLRPSF 345

QY 351 LLSNLQPNLTGARRLVEIIFGSRPRTSGPLCRTHSLSRRYWQMPRLFQQLVNNHAEQY 410  
 346 LLSSLRPSLSTGARRLVEIIFGSRPMPGTPRRLPRLPORTWQMPRLPFLLEQGNHQACPY 405

QY 411 VRLLRSHCRCFTANQVTDAL-----NTSPPHMMDLRLHSPQVQY 452  
 406 GVLKLKTHCPRLRA---VTPRAGVCAKEPKQPSVADEEDTDPRLVQLLRQHSPPWQY 462

QY 453 GFLRACIICKVYASLNGTRINERRFKNLKCPISLSKGYKGKLSLQELMWNKVKVBDCHWLRS 512  
 463 GFVRACLRRLVPPGLMGSRNERRFLNTKPKISLSKHKLSLQELTWKNSVRDCAWLRR 522

QY 513 SPGKDRVPAAHRLRERILATEFLKMDTYYVQLRSFFYTESTQKNLQFLFYYKRSVWS 572  
 523 SPGVGCPAAHRLRERILAKFLHNTMSVTVBLRSFFYETEQKNRNLFFYKRSVWS 582

QY 573 KLSQISGYQHQLSERVRLRSOEVRHHDQDTWLMPCRLRIPKNGLRLPVMMSYSMGT 632  
 583 KLSQISGTROHLKRVQRLSEAFVQHREARPALTSRLRIPKGDGLRPTVNMDFYVGA 642

QY 633 RALGHEKQAOAFTQTRLKTFLFSMLNVERTKPHLMSGSVLMNDIYTRTWRFLVRLRALDQ 692  
 643 RTFTRERKRAEFLTSVKAFLSVNLTERARRPGLLGSVGLDDIRHAWRTFVLRAQDP 702

QY 693 TPRMVTYKADYGAIDAIPOQKLYEVVANMTRHSESTYCYROYAVYRDRSGCQVKSFR 752  
 PT 703 PPELYVVKVNDVGTGADTIPDRLTIVTQYRVAQVQKAAGHGVRAKFS 761

QY 753 QVTTLSDQPMGQFLKHLQDSASALRNSWVIBSISNESSSSLFDFFLHFLRHSVVK 812  
 DB 762 HVSTLTDQPMYRQVHQAHLQET--SPLRDWVIEQSSSLNEASSGIFDVFLRMCHAVR 819

QY 813 IGDRRCYCTYQCGIPOQSSLSTLCSLCFGDMENKLPAEVQDGLLRLRFVDDFLVTPHLDQ 872

DB 820 IRGKSYVQCGIPOQSSLSTLCSLCYGMENKLPAIGRDRGLLRLVDDFLVTPHLD 879

QY 873 AKTFPLSTLVRGCVPEGTCMINIQLKTYUNPFPYBPGTIGGRAPYQLPPHCLFPWCGJLIDTQT 932  
 DB 880 AKTFPLTLYRVEPVGTCVNVNLKTYUNPFPYBPGTIGGRAPYQLPPHCLFPWCGJLIDTQT 939

		SQ	Sequence 1132 AA;
Qy	933 LEVFCDFSYGIAQTSIKTSITLQSFRAGKTMTRKLLSVRLKCHGLFLDQVNLSLQTYCI	992	Query Match 59.4%; Score 3505; DB 2; Length 1132;
Db	940 LEVQSDSYSTARTSRSASLIPNQGKFRAGMRRKLFQVRLKCSLFLDQVNLSLQTYCI	999	Best Local Similarity 62.4%; Pred. No. 0;
Qy	993 NIYKIPLLQAYRFHACVOLPFDQYRKNLTFGLIASSCYAIIKVNPNPNTLKS	1052	Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;
Db	1000 NIYKILLLQAYRFHACVOLPFDQYRKNLTFGLIASSCYAIIKVNPNPNTLKS	1059	Qy 1 MTRAPRCPAVRSILRSRYREWPLATFYRRLGPEGRRLYQPGDPKTYRTLVAQCLVCMHW 60
Qy	1053 GS---FPEAKHILCQFLKLAKHSVTKCLGPIRPAQKLLCRKPLRATMILKAA	1109	Db 1 MTRAPRCPAVRSILRSRYREWPLATFYRRLGPEGRRLYQPGDPKTYRTLVAQCLVCMHW 60
Db	1060 GAAGPLPSAVQWLCQFLKLTHRVTYVPLLSRLTAQTSRKLCPCTTLEAA	1119	Qy 61 GSQPPADLISFHQVSISLKELVARYVQLCERNERNVLAQFELLNEARGFELINEARGPPMAFTSSYR 120
Qy	1110 DPALSTDFTQFTLID 1122		Db 61 DARPAPPAESPRQVSCLKELVARYVQLCERGAKNVLAFGPAALDARGGPPEAFTTSYR 120
Db	1120 NPALPSDFKTLID 1132		Qy 121 SYLPNTVIELTRVSGAWMILLSPRGDDLYVLLAHCALYLVYPPSCAYOVCGSPLYQICA 180
			Db 121 SYLPNTVTDALRGSGAWGILLRQGDDLVHLLARCAFLVLPASCAQVCQGPPLYQICA 180
			Qy 181 TTDIWPSSASYRPTRPYGRNFTNLRFLQKIQSSRQBAKPLALPAPLSPGRTKHLSLSTSTS 240
			Db 181 ATDAPPPEAS-GPRRIG-----CERAWNHSVREAGVPGLPPAPCARRGGSARS 231
			Qy 241 VPSARKARCYCPVPRVEBGP-----HROVLPPTPSKSM-VPSPARSPEVPTAEKDLSKK 292
			Db 232 LPLERKPRRGAAPPEPERPTVQGQSSWAPCGRTRGSPDRGFCWVSPAR----PAEATSUB 286
			Qy 293 GKVSDSL-S-GSYCCXHKPSSTSLLSPRQNAFOLRP-FIETRFLFLYSRGDGOERLNPSF 350
			Db 287 GALGSTRHSHPSVGRQHAGPPSTSRRPPWDTPCPYPAETKHFLLYSSGD-KEQLRSPF 345
			Qy 351 LLSNQPNSTGARLVEIIFLGSRPTSGPLCRTLRLSRRYWMRPLFQQLVYHAECCY 410
			Db 346 LLSSSRPSPITGARLVEITFLGSRPWPMPCTPRLPRLPRLPRLPRLPRLPRLPRLPRLPRLPRLPRLPQLHNAQCPY 405
			Qy 411 VRLJLISHCFCRTANQVTDAL-----NTSPPHMDLRLIASSPQVY 452
			Db 406 GVLLKTHCPLRRA----VTPAAGYCAREKPKQGSVVAPEEEBDTDPRLVQLLRLQSSPQVY 462
			Qy 453 GFLRACLKVKVSASLWGTTRHNERPFRPKNLUKKPISLGKYGKSLSQBLMWYKMKVCECHWRS 512
			Db 463 GFVZACLRRLVPPSLWGSNNERERPLRNTKFCFISLGKHAKLSQLBLTWKMSVRDCAWLLR 522
			Qy 513 SPGKDVRPVAEHRLRERLATEFLWMDTYYVQLLRSPPVITESTFOKNRLFPYRKSWS 572
			Db 523 SPGVCVPAAEHRLRERLAKFLWMLMSVYVBLRSPPVTTETFOKNRLFPYRKSWS 582
			Qy 573 KLSIGTGVROHLERYVRLRELSQEVTRHHQDTWLAMPICLRLPKPKNGLRPIVNMYSMGT 632
			Db 583 KLSQSGTRQHKLKVQLRELSAEVTRQHREARPALTSRLRFPKDPGLRPIVNMDDYVVA 642
			Qy 633 RALGRRKQOHFTORLKLTFMSMLNVERTKPHMIGSSVLMNDIYRTWTAFLVRLRQLDQ 692
			Db 643 RTFRBECRABRLTSRKVLAFLSVNTERARRPGLIGASVGLDDIHTWATFTFVLVRQAQP 702
			Qy 693 TPRAYFVKADTVGAYDATAFOGKLVEVYANMIRHSESTYCIROAVVRDRISQGYIKSFR 752
			Db 703 PPELIVPKVDTGADTDIQQDRLTVETIASIK-BQNTYCVRYAVQKAHGHYTKAFKS 761
			Qy 753 QVTTISDLOPMGQFLKHQSDASALNSVVIQOSISMNESSSLFDFLHLRHSVVK 812
			Db 762 HVSTITDQPYMRFVHIIQET--SPLRDAVILQSSSLNEASSGGLFDVFLRMCHAVR 819
			Qy 813 IGDRCYTOCGIPQGSSSLTLLCSLCYGMENKLFAYFVORDGLLRLFVDDFLLYVTPHLDQ 872
			Db 820 IRGKSYVQCGIPQGSSSLTLLCSLCYGMENKLFAGIRDGLLRLVDDFLLYVTPHLDQ 879
			Qy 873 AKTFELSTLYHGVPEYGMINLQKTVNFVFBGTLGGAAQYQPLPAHCLEFWCGULLDDQT 932
			Db 880 AKTFELSTLYHGVPEYGMINLQKTVNFVFBGTLGGAAQYQPLPAHCLEFWCGULLDDQT 939
			Qy 933 LEVFDYDGYAQTSSIKTSITLQSFRAGKTMTRKLLSVRLKCHGLFLDQVNLSIQTVCY 992
			Db 940 LEVQDYSSTARTSIRASLTENRGEFKAGMRMRRCLFGVTLRKCHSLFLDQVNLSIQTVCY 999

RESULT 8  
AAW90251  
ID AAW90251 standard; protein; 1132 AA.  
AC AAW90251;  
XX DT 24-MAY-1999 (First entry)  
XX DE Human catalytic telomerase sub-unit protein.  
XX KW Human; catalytic telomerase subunit; therapy; diagnosis; hTC; assay;  
modulator; treatment; inhibit; cellular disorder; death; defect; cancer;  
ageing; antisense; neoplastic cell; telomerase-related condition;  
KW tumour cell.  
XX HOMO sapiens.  
XX PN WO9859040-A2.  
XX PD 30-DEC-1998.  
XX PP 09-JUN-1998; 98W0-EP003468.  
XX 20-JUN-1997; 97DDE-01026329.  
PR 26-MAR-1998; 98DB-0101324.  
PR 14-APR-1998; 98DB-0101646.  
XX PA (PARB ) BAYER AG.  
XX Hagen G, Siegmund H, Weichel W, Wick M, Zubov D;  
WPI: 1999-081276/07.  
N-PSDB: AAV72117.  
XX New catalytically active subunit of human telomerase - used in the modulation of telomerase activity, particularly for treating cancer and ageing.  
PT XX  
PS Claim 2: Fig 2; 76pp; German.

CC This sequence represents a novel human catalytic telomerase sub-unit (hTC). This protein can be used in screening assays to identify modulators of telomerase and to treat or inhibit cellular disorders, death, defects and/or other pathological processes involving telomerase, particularly cancer and ageing (also suitable for this are agents that stimulate, inhibit or mimic the activity of the subunit). Antisense nucleic acids inhibit telomerase action (by binding to specific mRNA), particularly in neoplastic cells and may be expressed *in vivo*. Antibodies and fragments of the protein, used as probes or primers, are used to diagnose telomerase-related conditions (especially neoplasia) by (i) detecting abnormal levels of the subunit protein in body fluids or tissues or (ii) by measuring the amount of the encoding nucleic acid. Expression of the nucleic acid encoding the subunit mRNA is confined to tumour cells, in contrast to the ubiquitous expression of the telomerase RNA subunit.

QY 993 NIYKFLQAYRFHACVIQLPFDQVRKNTLPEGLIISQASCCYAIUKVKNPGMTIKAS 1052  
 Db 1000 NIYKILLQAYRFHACVQLPFIQVWNKPTFFRVISSDTASLCYSLIKAKNAGMSLGAK 1059  
 QY 1053 GS--FPPEAAHHLCYAQAFLLKLAASHTYKCLGLGPLETAQKULCRKPEATMILKAA 1109  
 Db 1060 GRAGPLPSEAQNUCHAQAFLLKLTTRHTTYVPLIGSLRTAQTSRKRPGTITALEAA 1119  
 QY 1110 DPALSTDFTDFKILD 1122  
 Db 1120 NPALPSDFKILD 1132

RESULT 9  
 ID AAY288881 standard; protein; 1132 AA.  
 XX  
 AAY288881;  
 XX  
 AC  
 DT 17-JAN-2000 (first entry)  
 XX  
 DB Human telomerase reverse transcriptase protein.  
 XX  
 Human telomerase reverse transcriptase protein; hTRT; telomerase; hEST2;  
 KW catalytic protein component; cell proliferative capacity; DNA primer;  
 telomerase substrate; telomeric DNA synthesis; cell immortality;  
 neoplastic phenotype; diagnostic application; prognostic application;  
 KW telomerase related condition; cancer therapeutic agent;  
 KW telomerase expression; telomerase activity.  
 XX  
 OS Homo sapiens.  
 XX  
 Key Location/Qualifiers  
 Misc-difference 608  
 /note= "Corresponds to cac codon"  
 W09950279-A1.  
 XX  
 PD 07-OCT-1999.  
 XX  
 PF 31-MAR-1999; 99WO-US007160.  
 XX  
 PR 31-MAR-1998; 98US-00052919.  
 XX  
 PA (GERON CORP.  
 (UYTE-)  
 UNIV TECHNOLOGY CORP.  
 XX  
 Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;  
 PI Andrews WH;  
 XX  
 DR WPI: 1999-610834/52.  
 DR N-PSDB, AA208150.

XX  
 Antisense polynucleotides for human telomerase reverse transcriptase used  
 PT for diagnosing or treating cancer.  
 XX  
 PS Claim 2; Fig 2; 31pp; English.

XX  
 The present sequence is human telomerase reverse transcriptase protein.  
 CC This is the catalytic protein component of telomerase and is also  
 referred to as hEST2. hTRT has the ability to extend a DNA primer that  
 CC functions as a telomerase substrate for telomeric DNA synthesis. This  
 CC correlates with cell proliferative capacity, cell immortality, and the  
 CC development of a neoplastic phenotype. Human TRT antisense  
 CC oligonucleotides are useful for diagnostic or prognostic applications to  
 CC telomerase related conditions, including cancer. They are also useful as  
 CC therapeutic agents, for inhibition of telomerase expression and activity

XX  
 Sequence 1132 AA;

Query Match 59.4%; Score 3505; DB 2; Length 1132;  
 Best Local Similarity 62.4%; Pred. No. 0;

Matchee 719; Conservative 122; Mi matches 260; Indels 52; Gaps 13;  
 QY 1 MTRAPRCPAVRSILLRSRYREWPLATVRRJLGPEGRLLVQPGDPYTYRTLVAQCLVCMHW 60  
 Db 1 MTRAPRCPAVRSILLRSRYREWPLATVRRJLGPEGRLLVQPGDPYTYRTLVAQCLVCPW 60  
 QY 61 GSOPPAPDLSFIHOVSUKELYARVYORLCEERNERYLAFGPESLNEARGGPPMAFTSSR 120  
 Db 61 DARPPAPPSRQSVSUKELYARVYORLCERGAKVYLAFGAALDGARGGPPFAFTSSR 120  
 Db 121 SYLINTVETLRYSGAMILLSGRVDLVLVYLLAHCALYLLVPPSCAYQVCSPLXQICA 180  
 QY 121 SYLINTVETLRYSGAMILLSGRVDLVLVYLLAHCALYLLVPPSCAYQVCSPLXQICA 180  
 Db 121 SYLINTVETLRYSGAMILLSGRVDLVLVYLLAHCALYLLVPPSCAYQVCSPLXQICA 180  
 181 TTDIWPSSASYTRPTEPVGRFTNLREFLQOKSSRSOEAKPLAPLPERGTRKPHLSLTSTS 240  
 QY 181 ATQARPPHAS-GPRRLG-----CERAWNHSYVRBAGVPLGLPAPGARRGGSARS 231  
 QY 241 VPSAKKARCYPPYPRVBERGP-----HRQVLPTPSGSKSW-VPSPARSPPEVPAEKDLSK 292  
 Db 232 IPLPKRPRGGAPEPERTPVGGSSWAHPGRTRGSPDRGFCVSPAR-----PAEATSL 286  
 QY 293 GRVSDISLS-GSYCKKHKPSSTSLLSPRONAFOLP-FIETRFLYLSRGDCQBRNPSF 350  
 Db 287 GALSQTRHSHPSVGRQHAGPPESTSRPRPNDTPCPVYAAFKHFLYSSGD-KEQLRPSF 345  
 QY 351 LLSNLQPNLTGARRYVIIFLGSRSPITSGPLCRTHLSRRYQMRPLFOQLVNHACQY 410  
 Db 346 LLISSLRSLTIGARRYVIIFLGSRSPITGSPRPMGTPARLPLPQRTWQMRPLPFLIGLNHAQCPY 405  
 QY 411 VRLRSHSCHRFPTANQVTDAL-----NTSPPHIMDLIRLHSSPQVY 452  
 Db 406 GVLKLTCHCPLAA--VTPAAGVCALEKPKQSSVAAPBEEFDPRVQLQHQHSPPQVY 462  
 QY 453 GFLJRLACKYVSAISLNTRNERRFFKNLKKPISLSKYGKGLSLOQELMKWKFVEDCWLRS 512  
 Db 463 GFVRACLRLRYPGLGSSRNERRPLRNTKCPISLSKQHAKLSLQELUTWMSVDRCAWLRS 522  
 QY 513 SPGDQDPAEHLRERLATEFLWLMNDTYVQLRSFFYTTTESTFQKNRLFFYFKSVWS 572  
 Db 523 SPGVGCUPAAEHLRERLATEFLWLMNDTYVQLRSFFYTTTESTFQKNRLFFYFKSVWS 582  
 QY 573 KLOSIGVROHLERVRLRELSEEVHHDOTWLAMPICRLRPTPKPGLRPTVNMMSMGT 632  
 Db 583 KLOSIGVROHLERVRLRELSEEVHHDOTWLAMPICRLRPTPKPGLRPTVNMMSMGT 642  
 QY 633 RALGRRKQKAQHFTQRLKTLPSMLNVERTKPHLMGSSVLGRNDIYRTWAFVLRNALDQ 692  
 Db 643 RTFRERKRAEULTSRKALPSVNTERARRPGLLGASVGLDDIIRAWRTVLRRAQDP 702  
 QY 693 TPRMVFVKADYTGAYDAIPQGKLVETVANMTRHSESTCIRQAYVTRDSCQGVKSFR 752  
 Db 703 PPELYFKVDYTGATDIPQDLTETIASIK-PONTCYVRYAVQKAAGHVTKAFKPS 761  
 QY 753 QVTTLSDLQPYMGQFLKHLQDSDASLRNNTYEDISNMNESSSSLFDEPLHLSHVVK 812  
 Db 762 HVSTLTDLQPYMRQFVHLOFT--SPLRDVAVTBSOSSLNEASGFDPVAFRMCHAVH 819  
 QY 813 IGDRCTQCGIPOGSSLSLICSGMDMENKLPAEVQDGLLRLPFDDELLVTPHLDQ 872  
 Db 820 IRGKSTVYQCGIPOGSSLSLICSGMDMENKLPAEVQDGLLRLVDFLLVTPHLTH 879  
 QY 873 ARTFLSTLVRGVPEYFCMINIQKTVNFPYEPGTLGGAAPYQLPAHCLFPMCGLLDTQT 932  
 Db 880 AKTFPLRLVRGPEYFCVNLRKTVNFPYEDBAGGTAVQMPAGLFPWCGLIDTR 939  
 QY 933 LEVFDYSGAOTSITKTSITQSVFPAKTMKRNKLSLVPLKCHSFLDLOVNSLORYC1 992  
 Db 940 LEVQSDYSSARTSRSATLNRGPKRAGRNRCFGVLRKCHSFLDLOVNSLORYC1 999  
 QY 993 NIYKFLQAYRFHACVIQLPFDQVRKNTLPEGLIISQASCCYAILKVKNPGMTIKAS 1052  
 Db 1000 NIYKLLQAYRFHACVQLPFDQVWKNPTEFLRVSITASLCYSLIKAKNAGMSLGAK 1059

Qy 1053 GS---PPPEAAHMLCYOAPLKLAAHHSVYKCLIGPLRAQKLUCKRPEATMILKAA 1109  
 Db 1060 GAAGPILPSAVQWLCHQAPLKLKLRVTRVPLIGSLRATQTLRSLRCKLPTTLEAKA 1119

Qy 1110 DPALSTDPTQTLID 1122  
 Db 1120 NPALPSDPTQTLID 1132

RESULT 10  
 ID AAY2090 0 standard; protein; 1132 AA.  
 XX AAY2090;  
 XX 17-JAN-2000 (First entry)  
 XX DE Human telomerase reverse transcriptase (hTRT).  
 XX KW Telomerase reverse transcriptase; human; hTRT; cell proliferation; cancer.  
 XX OS Homo sapiens.  
 XX PN WO9950386-A2.  
 XX PD 07-OCT-1999.  
 XX PP 31-MAR-1999; 99WO-US007097.  
 XX PR 31-MAR-1998; 98US-00052864.  
 PR 03-AUG-1998; 98US-00123354.  
 XX (GERO-) GERON CORP.  
 XX PI Morin GB;  
 XX WPI; 1999-610842/52.  
 DR N-PSDB; ARI20279.

XX New catalytic polypeptide and polynucleotide, useful for increasing catalytic activity in a cell.

Claim 13; Fig 1; 24pp; English.

XX The present sequence represents human telomerase reverse transcriptase (hTRT). Human telomerase is a target for diagnosing and treating diseases relating to cell proliferation and senescence, such as cancer, or for increasing the proliferative capacity of a cell. A claimed method for increasing the proliferative capacity of a vertebrate cell, especially a human or other mammalian cell, involves introducing into the cell a recombinant hTRT polynucleotide encoding an hTRT variant in which residues 192-323, 192-271, 200-271, 222-323, 192-271 and 415-450 of the present sequence are deleted. A claimed method of preparing recombinant telomerase involves contacting a recombinant hTRT deletion mutant (as above) with a telomerase RNA component such that the 2 proteins associate to form a complex capable of catalysing the addition of nucleotides to a telomerase substrate. A claimed method for reducing telomerase activity in a cell involves introducing a recombinant polynucleotide encoding an hTRT variant having a deletion of amino acids 192-450, 560-565, 637-660, 638-660, 748-764 or 1051-1071 of the present sequence.

XX Sequence 1132 AA;

Query Match 59.4%; Score 3505; DB 2; Length 1132;  
 Best Local Similarity 62.4%; Pred. No. 0;  
 Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;

Qy 1 MTRAPRCPAVRSLLRSRYREWPLATEVRLGPGEGRLVQGDKLRYTVAQCLVCMHW 60  
 Db 1 MPRAPRCRAVRSLLRSRYREWPLATEVRLGPGEGRLVQGDKLRYTVAQCLVCMHW 60

Qy	1110 DPALSTDFTQTLID 1122	Qy	181 TTDIWPSSVASYRPTPVGRNFTNLRFQQIKSSROBAPKPLAQLPSRGTKHLSLTSTS 240
Db	1120 NPALEPSDFKTLID 1132	Db	181 ATQARPPHAS-GPERRLG----- CERAMHSYREAGYPLGLPAPGARRGGSRS 231
RESULT 1.1		Qy	241 VPSAKKARCYPVPRVEGP----- HRQVILPTPSGKSW-VPSPARSPEVPTAEKDLSK 292
AY443621		Db	232 LPPLKPRRGAAPBPERTPVGGSWAHPGRTRGPDGFCVSPAR---- PAEATSLB 286
ID	AY443621 standard; protein; 1132 AA.		
XX			
AC	AY443621;	Qy	293 GRVDSLISL-GSYCKHKPKSSPSLSSPRONAFOQLP-FIETRHFYLSRGDCQERLNPSF 350
XX		Db	287 GALSIGTRHSHPSVGRQHAGPESTISREPRWDTPCPVYAAETKHFYSSGD-KEVQLRPSF 345
DT	26-JAN-2000 (first entry)	Qy	351 LLSNLQNLNTGARRVBLIPIGSSRPTSGPLCRTHLSSRWTQMLPLFQQLLVNHAECQY 410
DB	A human telomerase reverse transcriptase (TRT) polypeptide.	Db	346 LLSLRLPSLTGARRVBLIPIGSSRPTSGPLCRTHLSSRWTQMLPLFQQLLVNHAECQY 405
XX		Qy	411 VRLRSHSCRFTANQVTDAL-----NTSPPHMIDLRLHSPQMVY 452
XX	Human; telomerase reverse transcriptase; TRT; T lymphocyte activation; dendritic cell; telomerase activity; cancer cell; proliferating cell; immunological destruction; telomerase; telomerase; cancer; proliferation disease.	Db	406 GVLKTHCPLRA---VTPANGVCAREKPOQSVAAPSEEDTDPRLVLQLRQHSPQMVY 462
OS	Homo sapiens	Qy	453 GFLRACLUCKYVSASLNLGTRNERRFKPNLKCPIISLCKYKGKLSLQELMWMKMKVEDCWLRS 512
PN	W0950392-A1.	Db	463 GFVRLCRLRRLVPGLGWSRNEERRFLRNLNTKCPIISLCKYKGKLSLQELMWMKMKVEDCWLRS 522
XX		Qy	513 SPGDQDRVPAEHLRERPLAFLFWLMDDTVVQLLRSPPFTTESTFQKNRLPFYRGSVWS 572
PD	07-OCT-1999.	Db	523 SPGVGCTPAAEHLRERPLAFLFWLMDDTVVQLLRSPPFTTESTFQKNRLPFYRGSVWS 582
XX		Qy	573 KLSQISGYRQHLERVLRLSQQEVRIHQDTWLMAMPICRLRPTKPNGLRPIVNMYSMGT 632
PF	30-MAR-1999; 99WO-US006898.	Db	583 KLSQISGIRQHLERVLRLSQQEVRIHQDTWLMAMPICRLRPTKPNGLRPIVNMYSMGT 632
XX		Qy	633 RALGRIKQAOQIFTORLKLTKLPSMLNVEKTKPHLMGSVVLGNDIVVTRTWAFLRVRALDQ 692
PR	31-MAR-1998; 98US-01120006P.	Db	643 RTFRERKRBALTSYKALFSLVNLNTRARRGLGASVGLDDINHAWRTFVLRVQDPD 702
PA	(GBRO-)	Qy	693 TPRMFYKADTYGDAIIPQKLVTTVANMIRHSESTYCTQYAVVFRDSCQVHKSPPR 752
XX	GERON CORP.	Db	703 PPELYFKVDTGAVVNTIPQRLTETIASIK-PONTYCYRRAVYQKAAGHVRVRAFKS 761
PT	PT	Qy	753 QVTTLSDLQPTMGOFKHLQDSDASALRNSVYIEQISMNESSLSDFPPFLHFLRHSVVK 812
PT	Biliciting an in vivo immune response for prevention and treatment of cancers.	Db	762 HVSTLTDLQPTMROFVHLQET--SPERDAVIEQSSLINEASGFLDFVFLRFMCHAVR 819
XX		Qy	813 IGDRCYTQCGIIPQGSSLSLULCSLCFGDMENKLPAFVGDRGLLRFVDDPFLVTPHLDQ 872
PS	PS	Db	820 IRGKSVVQCGIIPQGSSLSLULCSLCFGDMENKLPAFVGDRGLLRFVDDPFLVTPHLDQ 879
PS	Claim 1: 26pp; English.	Qy	873 AKTPFLSTLVRYGPEYGCMDINLQKTYUNPPVEPGTGGAAPYQPLPAHCLPPMCGLLDTQT 932
XX	The present sequence represents a human telomerase reverse transcriptase (TRT) polypeptide. The protein is used in the method of the invention. The specification describes a method for activating a T lymphocyte, comprising contacting the T lymphocyte with a dendritic cell that expresses a TRT peptide in the context of a MHC Class I or MHC Class II molecule. The protein causes induction of an in vivo immunological response to telomerase activity. Cancer cells are characterized by expression of endogenous TRT gene and the presence of detectable telomerase activity. Therefore, by eliciting a specific immune response to TRT or to TRT-expressing cells, it is possible to selectively target proliferating cells for immunological destruction. The method is used for eliciting an in vivo immune response to telomerase by activating a T lymphocyte, and is useful for prevention and treatment of cancers and other proliferation diseases/conditions.	Db	880 AKTFPLTFLVRSVPEYGCVNVLRKTVNFPVDEALGGTAVYQMPAHGLFPWCGLILDTQT 939
CC	Sequence 1132 AA;	Qy	933 LEVFCDYSGTAQTSKTSLTFQSVFAGKTMRNKQLSVLRLKCHGFLDLOQNSLQTCV1 992
CC		Db	940 LEVQSDYSSSTARTSFRASLTFNRRGFKAGRMRKKEGVLRLKCHSFLDLOQNSLQTCV1 999
CC		Qy	993 NIYKFLLQYRFHACVQIQLPFDQYRKRNTTFFLQGTTISQASCCYAILKVNPNQHILKAS 1052
CC		Db	1000 NIYKFLLQYRFHACVQIQLPFDQYRKRNTTFFLQGTTISQASCCYAILKVNPNQHILKAS 1059
CC		Qy	1053 GS---PPPEAAHWLTYQAPLKLAKHSVTKCLLQPLRQKLLRPLTAQKLLRPLTAQMTLKKAA 1109
CC		Db	1060 GRAGIPULSEAQWHLQYQAFUFLKLTHRVTVPLQGSLRTAQTSRKLPLTAQMTLKKAA 1110
CC		Qy	1110 DPALSTDFTQTLID 1122
CC		Db	1120 NPALSDFTQTLID 1132
CC		Qy	RESULT 1.2
CC		Db	AAV26580 AAV26580 standard; protein; 1132 AA.
CC		Qy	ID AAV26580
CC		Db	ID AAV26580 standard; protein; 1132 AA.





X New adult bone marrow-originated cells capable of differentiating into  
X heart muscle cells, applicable as remedies for various heart diseases  
X particularly with damaged heart muscle accompanying degeneration.  
X Disclosure: Page 128-134; 1589pp; Japanese.  
X The present invention relates to cells isolated from bone marrow, which  
X are capable of at least differentiating into heart muscle cells. The  
X cells are applicable as remedies for various heart diseases particularly  
X with damaged heart muscle accompanying degeneration. The present sequence  
X was used to illustrate the present invention.  
X Sequence 1132 AA:  
X

Query	Match	Score	DB	4:	Length	1132;
Best Local Similarity	62 4*;	Pred. No.	0;			
Matches	719;	Conservative	122;	Mismatches	260;	Indels
					52;	Gaps
					13	
1	MTRAPRCPAYRSLLRSRYEWPLATFVRRLGPBEGRLVQPGDPKLYRTLVAQCLVCMHW	60				
1	MPRAPCRAVESSLRSRYEWPLATFVRRLGPQGPRLVQGDPAFLRALVAQCLVCPV	60				
61	GSQPPIPDLSPHQVSSKELVARYWRLCERNERYLAFCFLNLLNARGGPPMATESSVR	120				
61	GSQPPIPDLSPHQVSSKELVARYWRLCERNERYLAFCFLNLLNARGGPPMATESSVR	120				
121	SYLPNTVIEFLRVSGAWMLLISRGDLYLVLAAHCLYLPPSCAYQVCGSPLYQICA	180				
121	SYLPNTVTDALRGSGAWMLLLRRVGDDVLVHLARCAFLVYAPSCAYQVCGPPYQLGA	180				
181	TTDIPVSASYRTRPVGRNFTNLRFLQOIKSSSRQEAQKPLAPLPSRGTRKHLSLSTS	240				
181	ATQAQPPHAS-GPERRLG-----CERAMWHSYREAGVPLGLPAGARRGGSASRS	231				
241	VPSAKKARCYFPVPRVEGP-----HRQVLPTPSGKSW-VPSPARSPVPTAEKDLSK	292				
232	LPLPGRPRGAPEPRTPVQGSMAHGPGRTRGPSPDGFCVSPAR-----PAEATSLS	286				
293	GRKVDISL-S-GSVCKXHKPSSTSLLSPRQNAFQLRP-FIETRHPFLYSRGDCQERLNPS	350				
287	GALSGTRRHSHPSVGQHHAGGPSTSREPRPNDTPCPVYASTKHFYSSGD-KEVLRPSP	345				
351	LLSNLOPENLTGARRYVBIIFUGJSRPTISGPLCRTHLSSRRYQWMPRLPQQLVNHABCQY	410				
346	LLSSLRPSLTGARRYVETIFUGJSRPTMMPGTPRRLPLPQRYQWMPRLPFLBLGHNHQCPY	405				
411	VRLJRSHCRPTANTQOYTDAL-----NTSPHIMLDLRLHSPMQVY	452				
406	GVLLKTHCPLEAA-----VTPAAGVCAREBKPOQSSVAAPPEBDIDPRLVQLRQHSPMQVY	462				
453	GFLRACLKCKVYASLNGTRHNRERRPKNLKKPFIISLGSKYKGKLSLQLQELMMKMKVEDCHWLRS	512				
463	GFVRACLRLYPPGLWGSREINRERRPLRNTKCPFIISLGSKHAKLSSLQELTWNKSVRDCAWLRR	522				
513	SPGDKDVPAAHRLRERIATFLWMDMTVQLLSSFFYTESTQKNRLPFFYRSVWS	572				
523	SPGVGCVPAAHRLRERIATFLWMDMTVQLLSSFFYTESTQKNRLPFFYRSVWS	582				
573	KLQSGICVROHLERVLRLSOBEVRIHQDTWMLAMPICRLRPTIPKNGLRLPIVNMNSMGT	632				
583	KLQSGICRQHLERVLRLSOBEVRIHQDTWMLAMPICRLRPTIPKNGLRLPIVNMNSMGT	642				
633	RALGRERKQAOQHFTQRLKTLFMSLMLYERTKPHLMGSSVGLGMNDIVYRTWFLRVRALDQ	692				
643	RTFREKRAERLTSRVLKPSVNTYERARRPGLLGAWSVGLGDDIHEAWRTFLRVRQADP	702				
693	TPRMFVKAQDVTGAYDAIPQKLVETVANMRHSESTYCIROAYVRRDSQCOQVHKSPPR	752				
703	PPELLFVKVDTGAYDTIPQDRLTETASILK-PQNTYCVRYAVVAAQKASGHVYCAFKS	761				
753	QVTLSDLOPQMGQFLKHLQDSASALRNSTVYIEQSTSMNNESSSSLSDFFLFLRHSSVVK	812				

Db	762	HVSTLTDLQPTARQPTAHLQET - SPLRDVAVIBGESSLNEASSGLFDVPLRFMCHAVR 812
Dy	813	IGDRCYTQCQGIPQGSSLSTLCSLCFGDMENKLPAEYQDGLLRLRFYDDELLVTPHLHDQ 872
Db	820	IRGKSTVQCQGIPQGSSLSTLCSLCFGDMENKLPAEYQDGLLRLRFYDDELLVTPHLTH 879
Dy	873	AKTFLSTLVRGVPEYQCMINLQKTVNPFYEPGTGGAAPYQVPHCLPPWCGLILDPTQ 932
Db	880	AKTFLATLVRGVPEYQCVNLRKTVNPFYEPDEALGGTAVQMPAHGLPPWCGLILDPTT 939
Dy	933	LEVFCDYSGTAQTSIKTSIATQSFQSVPAKTMRNKLSVLRKCHGFLDQVNSQTVCI 992
Db	940	LEVQSDISSTARSITASLIPNFGKAGRMRRKFGVLRKCHGFLDQVNSQTVCT 999
Dy	993	NIYKIPFLQAYRFHACVYIQLPDQYRKRNLTEFLGISSQASCYAILKVKNPGRMTLKAS 1057
Db	1000	NIYKIPFLQAYRFHACVYIQLPDQYRKRNLTEFLGISSQASCYAILKVKNPGRMTLKAS 1057
Dy	1053	GS--FPPEAAHILCQAFPLKLAHSVTKCLGSPLRTAQKLLRKLPATMTILKAAA 1108
Db	1060	GAAGGIPSEAVQWLHQAFPLKLTSHRTVTPYLLESLRATQTSRKLPSTTLYALEAAA 1119
Dy	1110	DPALSTDFQTILD 1122
Db	1120	NPALPSDKTILD 1132
RESULT 15		
AAB99930 standard; protein; 1132 AA.		
AAB99930;		
26-SEP-2001 (first entry)		
Human telomerase protein sequence SEQ ID NO:31.		
DB Human telomerase protein sequence SEQ ID NO:31.		
AC Homo sapiens.		
XX WO200148150-A1.		
XX 05-JUL-2001.		
XX 02-NOV-2000; 2000WO-JP007741.		
XX 28-DEC-1999; 99JP-00372826.		
XX 28-FEB-2000; 2000WO-JP011448.		
XX (KIOW ) KIOWA HAKKO KOGYO KK.		
XX Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;		
XX Yamada Y;		
XX WPI; 2001-425655/45.		
XX N-PSDB; AAI44366.		
XX Cells capable of differentiating into cardiomyocytes and originating in bone marrow or umbilical blood cells for study of cardiomyocyte differentiation and treatment of heart disease.		
XX Claim 146; Page 137-141; 187pp; Japanese.		
XX The present invention describes cells originating in bone marrow or umbilical blood cells which are capable of differentiating into cardiomyocytes. Also described are: (1) cardiomyocytes produced by the differentiation of the cells; (2) a method for carrying out the differentiation into cardiomyocytes, regulated by promotional and/or inhibitory factor; (3) a method for the differentiation of the cells into		
XX Claim 146; Page 137-141; 187pp; Japanese.		



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